AMENDMENTS TO THE CLAIMS:

Please amend claims 2, 4, 5, 7, 8, 19, 20 and 26. This listing of claims replaces all prior versions, and listings of claims, in the application.

LISTING OF CLAIMS:

1. (Original) A method for evenly distributing tags among members of a starting library, comprising:

a) optionally adjusting the diversity of a starting library so that the diversity is within an order of magnitude of the number of molecules in the library;

b) dividing the starting library into "n" sublibraries designated 1 to n, wheren n is equal to or less than the number of unique tags, wherein each unique tag specifically binds to a different capture agent;

c) attaching a tag to a plurality of members of each sublibrary to produce "n" tagged sublibraries containing tagged members, wherein each member has the same tag, and the tag is unique to each sublibrary;

d) mixing some or all of the tagged sublibraries to produce a mixed library, wherein the number of tagged molecules added from each sublibrary is the same; and

e) splitting the mixed library into "q" array libraries, wherein q is from 1 up to a predetermined number of arrays.

2. (Currently Amended) A method for evenly distributing nucleic acid molecules that encode polypeptide tags among members of a starting library, comprising:

a) optionally, adjusting the diversity of a starting library so that the diversity is within an order of magnitude of the number of members in the library;

b) dividing the starting library into "n" sublibraries designated 1 to n, wherein n is equal to or less than the number of different nucleic acid molecules having nucleic acid molecules encoding different polypeptide tags;

c) attaching a nucleic acid molecule encoding a polypeptide tag to members of each sublibrary to produce "n" tagged sublibraries containing tagged members, wherein the encoded polypeptide tag is unique to each sublibrary;

d) mixing some or all of the tagged sublibraries to produce a mixed library, wherein the number of tagged nucleic acid molecules added from each sublibrary is the same;

e) splitting the mixed library into "q" array libraries, wherein q is from 1 to a predetermined number of <u>array libraries</u> ~~arrays~~.

3. (Original) The method of claim 2, wherein the starting library is a nucleic acid library, and at step c) the polypeptide tag encoding portion of the tag is in reading frame with polypeptides encoded by the members of the sublibrary.

4. (Currently Amended) The method of claim 3, further comprising expressing the encoded polypeptides to produce tagged polypeptides in each array library.

5. (Currently Amended) The method of claim 3 ~~1~~, further comprising:

contacting the array libraries with 1 up to q collections of addressed capture agents under conditions in which the tags bind to the capture agents to produce 1 to q capture systems, wherein the capture agents at each locus in the addressed collection specifically bind to the same tag.

6. (Original) The method of claim 1, further comprising contacting array libraries with addressed capture agents, wherein agents at each addressed locus bind to the same polypeptide tag, thereby sorting the tagged molecules according to their tag.

7. (Currently Amended) The method of claim ~~1~~ 4, further comprising:

f) preparing up to "q" arrays from the array libraries.

8. (Currently Amended) The method of claim ~~3~~ 2 , wherein ~~the~~ tagged polypeptides are produced in each array library ~~are produced~~ by translation of nucleic acid molecules encoding tagged polypeptides.

9. (Original) The method of claim 1, wherein, on the average, each tagged molecule is unique in each array library.

10. (Original) The method claim 1, wherein the diversity of the starting library is about equal to the number of molecules in the library.

11. (Original) The method of claim 1, wherein the diversity of the starting library is about within about half an order of magnitude of the number of molecules in the library.

12. (Original) The method of claim 1, wherein the diversity of the starting library is with about 0.05 or 0.01 order of magnitude of the number of molecules in the library.

13. (Original) The method of claim 1, wherein the diversity of each sublibrary of tagged molecules is the about same.

14. (Original) The method of claim 13, wherein the diversity of each sublibrary of tagged molecules is within about 0.5 order of magnitude of all other tagged sublibraries.

15. (Original) The method of claim 13, wherein the diversity of each sublibrary of tagged molecules is within about 0.1 order of magnitude of all other tagged sublibraries.

16. (Original) The method of claim 13, wherein the diversity of each sublibrary of tagged molecules is within about 0.05 order of magnitude of all other tagged sublibraries.

17. (Original) The method of claim 13, wherein the diversity of each sublibrary of tagged molecules is within about 0.01 order of magnitude of all other tagged sublibraries.

18. (Original) The method of claim 2, wherein the polypeptide tag encoding portion of the tag is in reading frame with a polypeptide encoded by the nucleic acid molecule in the library.

19. (Currently Amended) The method of claim 2, wherein the nucleic acid molecule encoding the polypeptide tag is linked via a sequence of ~~nucleic acid molecules~~ nucleotides that encode an additional polypeptide linker to nucleic acid molecule members of the library.

20. (Currently Amended) The method of claim 1, wherein the diversity of the starting library is 10^2, 10^3, 10^4, 10^5, 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12} or greater.

21. (Original) The method of any of claim 1, wherein the diversity of the starting library is adjusted.

22. (Original) The method of 21, wherein the diversity is adjusted to be about equal to the number of molecules in the library.

23. (Original) The method of claim 21, wherein the diversity is adjusted to be within about 0.5 order of magnitude of the number of molecules in the library.

24. (Original) The method of claim 21, wherein the diversity is adjusted to about within an about 0.1 of an order of magnitude of the number of molecules in the library.

25. (Original) The method of claim 1, wherein the starting library is a nucleic acid library.

26. (Currently Amended) The method of claim 2~~1~~, wherein the starting library is a cDNA library.

27. (Original) The method of claim 3~~1~~, wherein the starting library encodes antibodies or fragments thereof or is comprised of antibodies or fragments thereof, wherein the antibodies or fragments thereof specifically bind to antigens.

28. (Original) The method of claim 3~~25~~, wherein the starting library encodes single-chain antibody fragments (scFvs).

29. (Original) The method of claim 5, wherein the capture system comprises tagged polypeptides bound to antibodies or fragments thereof.

30. (Original) The method of claim 29, wherein the antibodies or fragments that bind to tagged polypeptides comprise two polypeptide chains.

31. (Original) The method of claim 2, wherein:

the starting library is a nucleic acid library; and

the step of attaching a nucleic acid molecule encoding a polypeptide tag to molecules of each sublibrary is effected by cloning members of the nucleic acid sublibraries into sets of plasmids that comprise nucleic acid encoding the polypeptide tags;

there are up to "n" sets of plasmids;

each set of plasmids comprises nucleic acid that encodes a single polypeptide tag and each set encodes a unique polypeptide tag;

the molecules of each sublibrary are cloned into one set of plasmids, whereby the molecules of each sublibrary are tagged with the same tag-encoding nucleic acid, and each sublibrary is tagged with a unique tag-encoding nucleic acid.

32. (Original) The method of claim 31, further comprising transforming host cells with the sets of plasmids to produce sets of host cells; and maintaining them under conditions whereby the number of plasmids does not increase.

33. (Original) The method of claim 32, further comprising titering an aliquot of the transformed host cells from a plurality of sets of host cells that comprise tagged sublibraries.

34. (Original) The method of claim 32, further comprising normalizing the titer of plasmids in each of the tagged sublibraries in the sets of host cells so that the titer of each sublibrary is within 1, 0.5, 0.1, 0.05, or 0.01 order(s) of magnitude of the other tagged sublibrary titers.

35. (Original) The method of claim 34, wherein normalizing is effected by mixing sets of host cells.

36. (Original) The method of claim 35, further comprising splitting the mixed cells into from 2 to "q" equal portions.

37. (Original) The method of claim 34, further comprising expressing and purifying the tagged polypeptides encoded in the plasmids to produce from 1 to q array libraries of tagged polypeptides.

38. (Original) The method of claim 37, further comprising contacting the array libraries, with a corresponding number of addressed capture agents to produce from 1 to q capture systems.

39. (Original) The method of claim 31, wherein the nucleic acid library encodes a library of antibodies.

40. (Original) The method of claim 39, wherein the antibodies are ScFvs.

41. (Original) A collection of tagged molecules produced by the method of claim 1, wherein:

the starting library is a nucleic acid library or a polypeptide library; and

the tagged molecules comprise tagged polypeptides.

42. (Original) A capture system, comprising:

tagged polypeptides of claim 41; and

an addressable collection of capture agents, wherein:

each locus in the collection contains capture agents that specifically bind to the same tag; and

the tagged molecules are specifically bound to capture agents.

43. (Original) A capture system, comprising:

an addressable collection of capture agents, wherein each locus in the collection contains capture agents that specifically bind to the same polypeptide tag, wherein the tags are evenly distributed among the tagged polypeptides;

a plurality of different polypeptide-tagged molecules bound to the capture agents, wherein the polypeptide-tagged molecules are sorted according to their specificity for the capture agents, wherein the tags are evenly distributed among the tagged molecules such that the diversity of tagged molecules at each locus in the collection is within one order of magnitude between and among loci.

44. (Original) A capture system, comprising:

an addressable collection of capture antibodies, wherein each locus in the collection contains antibodies that specifically bind to the same polypeptide tag;

a plurality of different polypeptide-tagged antibodies or fragments thereof bound to the capture antibodies;

wherein the polypeptide-tagged antibodies or fragments thereof are sorted according to their specificity for the capture antibodies; and

wherein the tags are evenly distributed among the tagged polypeptides such that the diversity of tagged molecules at each locus in the collection is within one order of magnitude.

45. (Original) The capture system of claim 42, wherein the diversity of tagged molecules at each locus in the collections is within 0.05 or 0.01 order of magnitude between and among loci.

46. (Original) The capture system of 42, wherein each locus in the capture system further comprises an additional agent or plurality thereof at one or more loci, wherein the additional agents are common to a plurality of loci, and bind to and/or interact with captured biological particles and/or captured molecules.

47. (Original) The capture system of claim 46, wherein a plurality of additional agents are added.

48. (Original) The capture system of claim 46, wherein the amounts of the additional agents vary from locus to locus.

49. (Original) The capture system of claim 46, wherein the additional agents are selected from the group consisting of antibodies known to bind to captured biological particles and molecules, adhesion molecules, drugs, receptors, enzymes and combinations thereof

50. (Original) The capture system of claim 46, where the additional agent serves to anchor molecules and/or biological particles, to act as a co-stimulatory molecule, to bind to surface receptors different from the first capture agents, to exert a biological effect, to further select the biological particles and/or captured molecules. That bind to a locus.

51. (Original) The capture system of claim 46, wherein the additional agent is selected from the group consisting of trastuzumab and rituximab.

52. (Original) The capture system of claim 46, wherein the diversity of tagged molecules at each locus in the collection is within 0.5 order of magnitude or is within 0.1 order of magnitude.

53. (Original) The capture system of claim 42, wherein the polypeptide tagged molecules or polypeptides are polypeptide-tagged single-chain antibody fragments (scFvs).

54. (Original) A capture system, comprising:

a collection of tagged molecules produced by the method of claim 1; and

an addressable collection of capture agents, wherein:

each locus in the collection contains capture agents that specifically bind to the same tag;

the tagged molecules are specifically bound to capture agents; and

the diversity of tagged polypeptides or tagged molecules is 10^3, 10^4, 10^5, 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12} or more.

55. (Original) A collection of tagged molecules, wherein:

the tags are evenly distributed among the tagged molecules such that the number of molecules having each tag is within 1.0, 0.5, 0.1, 0.05, or 0.01 order of magnitude; and

the collection has a diversity of at least 103.

56. (Original) The collection of claim 55 that has a diversity of at least 10^4.

57. (Original) The collection of claim 55 that has a diversity of at least 10^5.

58. (Original) The collection of claim 55 that has a diversity of at least 10^6.

59. (Original) The collection of claim 55 that has a diversity of at least 10^7.

60. (Original) The collection of claim 55 that has a diversity of at least 10^8.

61. (Original) The collection of claim 55 that has a diversity of at least 10^9.

62. (Original) The collection of claim 55 that has a diversity of at least 10^{10}.

63. (Original) The collection of claim 55, wherein the collection is a nucleic acid library.

64. (Original) The collection of claim 55, wherein the collection is a nucleic acid library tagged with oligonucleotides that encode polypeptide tags.

65. (Original) The collection of claim 55, wherein the collection is tagged with polypeptide tags.

66. (Original) The collection of claim 55, wherein the collection comprises polypeptides tagged with polypeptide tags.

67. (Original) The collection of claim 64 that is an addressable collection, wherein the diversity of different tagged molecules at each locus in the array is within one order of magnitude.

68. (Original) A capture system, comprising capture agents; and

a collection of claim 55 bound thereto.

69. (Original) A method for capturing molecules, comprising:

contacting a capture system with molecules under conditions whereby molecules bind to the capture system, wherein:

the capture system comprises a plurality of addressed loci;

the capture system comprises an addressed collection of polypeptide-tagged molecules bound to addressed capture agents at each locus;

the capture agents at each locus bind to the same polypeptide tag;

the polypeptide tag to which the capture agent binds is different among the loci;

each locus in capture system contains a plurality of different molecules each with the same tag bound to the capture agents; and

the polypeptide tags are evenly distributed among the tagged molecules such that the diversity of tagged molecules at each locus in the capture system is within one order of magnitude.

70. (Original) The method of claim 69, wherein the diversity of tagged molecules among the loci is within 0.5 order of magnitude.

71. (Original) The method of claim 69, wherein the diversity of tagged molecules among the loci is within 0.1 order of magnitude.

72. (Original) The method of claim 69, wherein the diversity of tagged molecules among the loci is within 0.05 or 0.01 order of magnitude.

73. (Original) The method of claim 69, wherein the tagged molecules are polypeptides.

74. (Original) The method of claim 69, wherein the tagged molecules comprise tagged nucleic acid molecules.

75. (Original) The method of claim 69, wherein the tagged molecules comprise tagged antibodies or fragments thereof.

76. (Original) The method of claim 75, wherein the polypeptide tagged antibodies or fragments are polypeptide-tagged single-chain antibodies (scFvs).

77. (Original) The method of claim 69, wherein the tagged molecules comprise a library of molecules.

78. (Original) The method of claim 77, wherein the library is an antibody library or a library of nucleic acid molecules encoding an antibody library.

79. (Original) The method of claim 77, wherein the library is an scFv library or a nucleic acid library encoding the scFvs.

80. (Original) The method of claim 69, wherein the capture agents comprise polypeptides or nucleic acids or analogs thereof.

81. (Original) The method of claim 69, wherein the capture agents comprise receptors, ligands, drugs, enzymes, or enzymes that are modified to have reduced catalytic activity.

82. (Original) The method of claim 69, wherein the capture agents comprise antibodies or fragments thereof.

83. (Original) The method of claim 69, wherein the capture system comprises a positionally addressable array.

84. (Original) The method of claim 83, wherein the capture agents are immobilized at discrete loci on a solid support.

85. (Original) The method of claim 84, wherein the solid support is selected from the group consisting of silicon, celluloses, metal, polymeric surfaces, and radiation grafted supports.

86. (Original) The method of claim 84, wherein the support comprises a well or a pit or plurality thereof in a surface of the solid support.

87. (Original) The method of claim 69, wherein the capture agents are addressably tagged by linking them to electronic, chemical, optically or color-coded labels.

88. (Original) The method of claim 87, wherein the labels comprise particulate supports.

89. (Original) The method of claim 88, wherein the particulate support is selected from the group consisting of silicon, celluloses, metal, polymeric surfaces and radiation grafted supports.

90. (Original) The method of claim 88, wherein the particulate support is selected from the group consisting of gold, nitrocellulose, polyvinylidene fluoride (PVDF), radiation grafted polytretrafluoroethylene, polystyrene, glass and activated glass.

91. (Original) The method of claim 69, wherein the tagged molecules have a diversity of at least about 10^2, 10^3, 10^4, 10^5, 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12} or greater.

92. (Original) The method of claim 69, wherein each locus in the capture system further comprises an additional agent or plurality thereof at one or more loci, wherein the additional agents are common to a plurality of loci, and bind to and/or interact with the captured biological particles and/or captured molecules.

93. The method of claim 92, wherein a plurality of additional agents are added.

94. (Original) The method of claim 92, wherein the amounts of the additional agents vary from locus to locus.

95. (Original) The method of claim 92, wherein the additional agents are selected from the group consisting of antibodies known to bind to the captured biological particles and/or captured molecules, adhesion molecules, drugs, receptors, enzymes and combinations thereof.

96. (Original) The method of claim 92, wherein the additional agent is selected from the group consisting of trastuzumab and ritimab.

97. (Original) The method of claim 69, wherein the molecules comprise biological particles; and wherein the biological particles are cells selected from the group consisting of immune cells, neurons, cancer cells, bacterial cells and infected cells.

98. (Original) The method of claim 69, wherein the molecules are biological particles selected from the group consisting of subcellular compartments, organelles, viral particles and pathogens.

99. (Original) The method of claim 69, wherein the cells are dendritic cells, T cells, or B cells.

100. (Original) The method of claim 69, wherein the capture agents are cell surface receptors, T cell receptors, MHC peptides, MHC peptide complexes, B cell receptors, ICAMs, Toll-like receptors, PPAR ligands, ion channels, chemokine receptors, nicotinic acetylcholine receptors, dopamine receptors, muscarinic receptors, small molecule receptors, ICAMs, TNF receptors, interleukin receptors, BCAMS, or interferons.

101. (Original) The method of claim 69, further comprising:
assessing the effects of capture on a captured molecule or plurality thereof.

102. (Original) The method of claim 101, wherein the effect is selected from the group consisting of a change in structure, a change in activity, a physical change, and a chemical change.

103. (Original) The method of claim 101, wherein an effect is detected by visualizing the captured molecules.

104. (Original) The method of claim 101, wherein an effect is detected by staining or labeling captured molecules.

105. (Original) The method of claim 69, further comprising:
detecting or identifying captured molecules.

106. (Original) The method of claim 105, wherein identification is effected by staining or visualizing captured molecules.

107. (Original) The method of claim 69, wherein the molecules are labeled prior to capture.

108. (Original) The method of claim 69, further comprising: identifying tagged molecules that capture the molecules.

109. (Original) The method of claim 69, further comprising: identifying tagged molecules that capture labeled molecules.

110. (Original) The method of claim 106, wherein the stain specifically reacts with a one or a plurality of the captured molecules.

111. (Original) The method of claim 106, wherein a plurality of stains are applied.

112. (Original) The method of claim 111, wherein one stain reacts with a feature common to all molecules of a particular type, and at least one other stain reacts with a subset thereof.

113. (Original) The method of claim 106, wherein a stain is selected from the group consisting of fluorescent dyes, luminescent labels, enzyme labels, and immunostains.

114. (Original) The method of claim 106, wherein a stain is are selected from the group consisting of green fluorescent protein, red fluorescent protein, blue fluorescent protein, an immunostain and semiconductor crystals.

115. (Original) The method of claim 69, wherein contacting is performed in the presence and absence of a test compound, and the results are compared to identify test compounds that alter binding of molecules to the capture system.

116. (Original) The method of claim 69, further comprising:

adding a test compound or exposing the capture system to a condition before, during or after contacting the capture system with the molecules; and after contacting assessing the effects of the test compound on the captured molecules.

117. (Original) A method for identifying modulators of interactions between capture systems and molecules, comprising:

a) performing the method of claim 69;

b) adding a test compound or exposing the capture system to a condition before, during or after contacting the capture system with molecules or before, during or after contacting the capture agents with the tagged molecules; and

c) identifying a change in an interaction of the molecules with the capture system or tagged molecules with the capture agents to identify a test compound that modulates the interaction between the molecules and the capture system or between tagged molecules and capture agents.

118. (Original) The method of claim 117, wherein the change is assessed by detecting a change in binding pattern or a physical or chemical change in the bound molecules or a conformational change in the bound molecules and/or tagged molecules.

119. (Original) A method of sorting molecules or reducing the diversity thereof, comprising:

a) contacting a collection of tagged molecules with an array of addressed capture agents, wherein:

the agents at each addressed locus specifically bind the same tag, which differs from the tag to which agents at other loci bind;

the tags are evenly distributing among the tagged molecules; and

on the average, each tagged molecule is unique in each array library;

b) identifying from among the tagged molecules those having a predetermined activity or property;

c) based upon the tag(s) of the identified molecules, identifying the molecules linked to the tag, thereby sorting the molecules based upon the tag.

120. (Original) A method of reducing the diversity of a collection of molecules, comprising:

a) contacting a collection of tagged molecules with an array of addressed capture agents, wherein:

the agents at each addressed locus specifically bind the same tag, which differs from the tag to which agents at other loci bind;

the tags are evenly distributing among the tagged molecules; and

on the average, each tagged molecule is unique in each array library;

b) identifying from among the tagged molecules those having a predetermined activity or property;

c) based upon the tag(s) of the identified molecules, identifying the molecules linked to the tag;

d) selecting the molecules linked to the tag, thereby reducing the diversity of the collection of molecules.

121. (Original) The method of claim 2, further comprising:

contacting the array libraries with 1 up to q collections of addressed capture agents under conditions in which the tags bind to the capture agents to produce 1 to q capture systems, wherein the capture agents at each locus in the addressed collection specifically bind to the same tag.

122. (Original) The method of claim 2, further comprising contacting array libraries with addressed capture agents, wherein agents at each addressed locus bind to the same polypeptide tag, thereby sorting the tagged molecules according to their tag.

123. (Original) The method of claim 1, further comprising:

f) producing a capture system from each array library by contacting members of the array library with addressable collections of capture agents.

124. (Original) The method of claim 2, further comprising:

f) producing a capture system from each array library by contacting members of the array library with addressable collections of capture agents.

125. (Original) The method of claim 2, further comprising:

f) preparing up to "q" arrays from the array libraries.

126. (Original) The method of claim 2, wherein, on the average, each tagged molecule is unique in each array library.

127. (Original) The method of claim 2, wherein the diversity of each sublibrary of tagged molecules is the about same.

128. (Original) The method of claim 2, wherein the diversity of the starting library is 10^2, 10^3, 10^4, 10^5, 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}or greater.

129. (Original) The method of any of claim 2, wherein the diversity of the starting library is adjusted.

130. (Original) The method of 129, wherein the diversity is adjusted to be about equal to the number of molecules in the library.

131. (Original) The method of claim 2, wherein the starting library is a cDNA library.

132. (Original) The method of claim 2, wherein the starting nucleic acid library encodes single-chain antibody fragments (scFvs).

133. (Original) The collection of claim 65 that is an addressable collection, wherein the diversity of different tagged molecules at each locus in the array is within one order of magnitude.

134. (Original) The collection of claim 66 that is an addressable collection, wherein the diversity of different tagged molecules at each locus in the array is within one order of magnitude.